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OM nucleic - nucleic search, using sw model

Run on: February 16, 2003, 17:00:49 ; Search time 193.217 Seconds  
(without alignments)  
10829.323 Million cell updates/sec

Title: US-09-497-967-3

Perfect score: 1404

Sequence: 1 atgaataataatttttagt.....tgattttattattattatta 1404

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2773584 seqs, 745158349 residues

Total number of hits satisfying chosen parameters: 5547168

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_NA\_New.\*  
1: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77.4	5.5	897	6	US-10-144-771-39592
2	65.4	4.7	961	6	US-10-144-771-31796
3	60	4.3	1635	6	US-10-203-138A-8641
4	60	4.3	1973	6	US-10-203-138A-3500
5	53.4	3.8	1188	6	US-10-144-771-4034
6	52.2	3.7	510	6	US-10-203-138A-7146
7	50	3.6	1248	6	US-10-092-411A-1120
8	49	3.5	1141	5	US-09-806-708B-22
9	48	3.4	3532	6	US-10-017-161-1913
10	47.4	3.4	1954	6	US-10-144-771-4707
11	45.8	3.3	1075	6	US-10-203-138A-7632
12	45.8	3.3	1403	6	US-10-203-138A-2529
13	45.8	3.3	3489	6	US-10-194-046-1
14	45.8	3.3	11091	6	US-10-092-411A-2243
15	45	3.2	21423	5	US-09-949-004-601
16	44.4	3.2	583	6	US-10-144-771-29725
17	43.4	3.1	1231	6	US-10-017-161-2047
18	43.2	3.1	38918	6	US-10-017-161-2049
19	43.2	3.1	428573	5	US-09-948-124-119
20	42.8	3.0	439	6	US-10-203-138A-8573
21	42.8	3.0	1664976	5	US-09-692-570-1
22	42.2	3.0	1805	6	US-10-144-771-22890
23	42.2	3.0	7040	6	US-10-311-506-48
24	42.2	3.0	7040	6	US-10-311-507-48
25	42.2	3.0	2323866	5	US-09-948-124-64
26	42	3.0	574	6	US-10-203-138A-227

27	42	3.0	3673778	6	US-10-312-841-1	Sequence 1, Appl
28	41.8	3.0	756	7	US-60-434-832-6082	Sequence 6082, Ap
29	41.6	3.0	729	6	US-10-144-771-31479	Sequence 31479, A
30	41.6	3.0	1118	6	US-10-144-771-33054	Sequence 33054, A
31	41.6	3.0	1141	5	US-09-806-708B-22	Sequence 22, Appl
32	41.2	2.9	203	5	US-09-531-113-35330	Sequence 35330, A
33	41.2	2.9	1083	5	US-09-950-084-2103	Sequence 2103, Ap
34	41.2	2.9	1372	6	US-10-017-161-2245	Sequence 2245, Ap
35	41.2	2.9	3275	6	US-10-144-771-21113	Sequence 21113, A
36	41.2	2.9	5912	6	US-10-311-455-575	Sequence 575, App
37	41.2	2.9	74105	5	US-09-950-084-7446	Sequence 7446, Ap
38	41.2	2.9	580073	4	US-08-545-528D-1	Sequence 1, Appl
39	41	2.9	489	6	US-10-203-138A-5026	Sequence 5026, Ap
40	41	2.9	1278	6	US-10-092-411A-58	Sequence 58, Appl
41	41	2.9	2297	5	US-09-724-676-30403	Sequence 30403, A
42	41	2.9	2297	5	US-09-724-676-30403	Sequence 30403, A
43	41	2.9	2348	5	US-09-724-676-30401	Sequence 30401, A
44	41	2.9	2348	5	US-09-724-676-30401	Sequence 30401, A
45	41	2.9	2732	5	US-09-724-676-30402	Sequence 30402, A

## ALIGNMENTS

## RESULT 1

US-10-144-771-39592

; Sequence 39592, Application US/10144771

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig

; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF

; FILE REFERENCE: CLO01321

; CURRENT APPLICATION NUMBER: US/10/144.771

; CURRENT FILING DATE: 2002-05-15

; NUMBER OF SEQ ID NOS: 47235

; SEQ ID NO 39592

; LENGTH: 897

; TYPE: DNA

; ORGANISM: HUMAN

US-10-144-771-39592

Query Match

Best Local Similarity 5.5%; Score 77.4; DB 6; Length 897;

Matches 330; Conservative 0; Mismatches 421; Indels 0; Gaps 0;

QY	222	TCCTGGTGTAAACCAATCCACCTGCTACTGCTAAATTTAGTCACATAATGTAACGTTAA	281
Db	135	TCCTACTGCTACAGCTTCTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTAC	194
QY	282	ATGCGCTGCTGCTACCGCAATTCGAGTGGAGCAACAGATTATGCACATAATACACAGA	341
Db	195	TCCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTAC	254
QY	342	ATGCTTTAATGTAGAAATTAATTTTATAATGAAATGCTCCAAATTTTAAATGCAGTGC	401
Db	255	TCGTACAGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTAC	314
QY	402	TAGTACATGCACAGCTTTCGGTAAACAGATTGGTGGTGCATGCTACTGCTGGTAAATGC	461
Db	315	TCGTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTAC	374
QY	462	CGTACCATTAGTCGCAATGTAACGTCGATGTCCTACTGCTACTGCTACTGCTACTGCTAC	521
Db	375	TCGTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTAC	434
QY	522	AGTAACACTGATTTATGTTAGATTCATTCACAGATGTTTAAATGTAGACTTAACTTTTA	581
Db	435	TCGTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTAC	494
QY	582	CTAATAGGTAAATGGAATATCTCTTTCAATCAGGTAAAGTTAATGACACACCTTG	641
Db	495	TCGTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTACTGCTAC	554
QY	642	TCCGGCAATTAACCTGCTAATGTTGCTTAAAGCTACTTTAGGTAAATGATGCTACAATAC	701





D	b		1104	TGATGGTGATGGTGTGCTGCTAGTCATGGTGGTGGTGGTGGTAGTGATGG	1045
Q	y		537	TGTTAGATCAATCAGAAATGTTTAATCTAGACCTTAACCTTTACTATAATGGTAATAA	596
D	b		1044	TGGTGGTGGTGTAGTGAATGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	985
Q	y		597	TGTAATACTCCCTTCCAATCCAGGTAAAAAGTAAATGCACACCCTTGTGCCGCAATTAAACC	656
D	b		984	TGGTAGTGAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	925
Q	y		657	TGCTAATGTTGGTTAAGCTACTTTAGGTAAATGCTACAATAACCCCATAAATGCTAACGT	716
D	b		924	TGCTAGTGAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	865
Q	y		717	TGCATGCCCTGATGGTFACTATAAGTGCCTGCGAGAGAATAAATTTGGGTAGCACAAAACAC	776
D	b		864	TGGTAGTGAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	805
Q	y		777	TGAATGACTAAATGTGTCCTCACTTTTACAATAAATAATGCTCCTTAATTTCAATCCAGG	836
D	b		804	TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	745
Q	y		837	TAATAGTACATGCTACCTTGCCTGCCCAGCAAATAAGAGTATGTGCTSAAGCCATGCAGG	896
D	b		744	TAGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	685
Q	y		897	TGTTGCCGCTACTTTTAGCCAAATAATGTAATTTGCATGCCCTGATGCTACTGCAATTGC	956
D	b		684	TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	625
Q	y		957	TAGTGGAGCAACTAAATATGTAATAATATAAACACAAATGCTAAATTTGCTGCTFAACTT	1016
D	b		624	TGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	565
Q	y		1017	TTATTTTTGATGGTAATAAATTTAGCAGAGAAGTAGTAGATCAARAGCATGCCAGCAA	1076
D	b		564	TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	505
Q	y		1077	TAAAGTTTAAGGCGCTGTAGCAACTGCAGTGCCTGCTACTGCTACTTTAAATTCGCAATAATGTC	1136
D	b		504	TAGTGGTTGTAGTAGTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	445
Q	y		1137	COTTTAGTGCCTCTGCTACTGTACTGTACCTACCCGATGG	1172
D	b		444	TGGTGAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	409
RESULT 5 US-10-144-771-4034/c ; Sequence 4034, Application US/10144771 ; GENERAL INFORMATION: ; APPLICANT: VENTER, J. Craig ; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF ; FILE REFERENCE: CL001321 ; CURRENT APPLICATION NUMBER: US/10/144,771 ; CURRENT FILING DATE: 2002-05-15 ; NUMBER OF SEQ ID NOS: 47235 ; SEQ ID NO 4034 ; LENGTH: 1188 ; TYPE: DNA ; ORGANISM: HUMAN ; US-10-144-771-4034					
Query Match                  3.8%; Score 53.4; DB 6; Length 1188; Best Local Similarity      42.4%; Pred. No. 0.0088; Matches 288; Conservative    0; Mismatches 391; Indels     0; Gaps        0;					
Qy		56	AATCTGCTAATTTGCTGTTTGGAACTGAAACTAACACACCCGGATAAGTTGATGATCTAG	115	
D	b	1101	AAGCTGGTGGTGGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1042	
Qy		116	GAACTCCTGC AAATTTGTGTAATTGTAG AAAA ACTTTTATATAATAA TCGTCTGCTT	175	



Thu Feb 20 11:10:18 2003

Db 139 HHYVTAMNNAWTTMCMDKDDKRTWWKKNNNATGWDDDTKYHMNNNCCBTVWVRY 198  
Qy 303 TCCAGGTGGAGCAACAGATTATGACGCAATAATACAGAAATGCTTAATTTGTAGAATAA 362  
Db 199 KTRDWSBKRNNGYGBWKKNSYDVTYWWDDCKRKYRVRVTRGRMRNVMWABTA 258  
Qy 363 TTTTATATGAAATGCTCCAAATTTAATGCGAGGTGCTAGTACATGACACCTGTGCC 422  
Db 259 HRRYNNNGWTBAMAYRRWTNNNNNAKMKCRKAKYWGWRBVBVNST-CTTWKSKTKVR 317  
Qy 423 GGTAAACAGAGTGTGTGCTGATTGACTGCTGGTAATGCGCGTACCATAGTCGCATAATG 482  
Db 318 TSCWANNCRAGDANKDHKKWKSAAAGYVNNNNNNNNWTKKARHBAWVWHSAAWKW 377  
Qy 483 TAAGTGGCATGCTCTACTGCTACTGCTACTGATGATGAGTAACTACTGATTATGTTAG 542  
Db 378 HANAHSRKKWTBYKRTVMVNNNGTTMMKRWMAWYWKMDMBGTYNNNNNGRYYG 437  
Qy 543 ATCATTACAGAAATGTTAAATGTAGACTTAACCTTTTACTATATAATGTAATGTA 602  
Db 438 WTKKKWWTYYKWKANCKWRADWHTCHNNTTWKKMTYNNNCYKWSMTNGKSHRBA 497  
Qy 603 TACTCCTTTCAATCCAGGTAAAGTTAATGACACACTTGTCCGGCAATTAACACTGTAA 662  
Db 498 AVITWVWRRYAHANNNDYWWKACTWYKYBVCWKWNNYAATWTKSSWNTSRYYR 557  
Qy 663 TGTGCTTAAGTACTTTAGTAAATGATGCTACATAACCCATAATGTAACGTGTGATG 722  
Db 558 WKTNSWRSDTRSMGRANNYARABHYKYKWRWBWSHTWBHBRAGAHHYWBMMYB 617  
Qy 723 CCTGATGCTACTATAAGTCTGCTGGAGTAAATAATTTGGTGACACAAAACCTGAATG 782  
Db 618 AKCHMKAWTKAKKYAGAGSNNNNNNNNNNNNNNNNATCARDDYYAASRYVAMANAKWY 677  
Qy 783 TACTAATGTCCTCACTTTTACAAATAATGCTCTAATTTCAATCCAGGTAATAG 842  
Db 678 YKBAANNAYTHANNWGCWNNATDTRTMKNNNNNNNAGTWKNNNNNNNAKNSAAKNY 737  
Qy 843 TACATGCTACCTGCGCCAGCAATAAGATTATGCTGCTGAAGCCACTGCAGGTGTGC 902  
Db 738 AAAAVKAAKXHWANKWAMRGHWAADAAATTDKRNNGAYTKYTTNNNNNTYRGVVTNTA 797  
Qy 903 CGCTACTTTAGCCAAATAATGTAATGCTGCCCTGATGCTAGTGCATTTGCTAGTGG 962  
Db 798 ARDGMNNNNNNNNNNNNNNNGWSMDMVWVAVANYGTNNNNNNNNNNAYAWNTKWTYT 857  
Qy 963 AGCAACTAATTAATGTAATATAACAGAAATGCTTAATG-----TGCTGCTAACT 1015  
Db 858 DRRRBAYTNN 917  
Qy 1016 TTTATTTGATGTAATAATTTCTAGCGAGGAAGTAGTAGTGCAGCAAGCATGCCAGCAA 1075  
Db 918 NNN 977  
Qy 1076 ATAAGTTTAAGCGCTGTAGCACTGCGAGGTGATGCTACTTCTAATGCTAATGTTG 1135  
Db 978 CTWYTWMTTTRTYAATRWKTNNTATGSMTRCNAIGKNNNNYTWGKTRWTYRMAIRWM 1037  
Qy 1136 CCCTGAATGCCCTGCTGCTAGTACTACTACCGATGGAACAACATCTACTTATAATAAG 1195  
Db 1038 KAMKVMATGSMNTSARWYAKTRAYKGYNNACAWRWGRKATCYMTDNNWWTACATIS 1097  
Qy 1196 CAGCATCTGAATGTGTTAAATGTGCTGCCAA 1226  
Db 1098 WMATHYNNHHCKNN 1128

RESULT 9  
US-10-017-161-1913  
; Sequence 1913, Application US/10017161  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI

; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 084335/0152  
; CURRENT APPLICATION NUMBER: US/10/017,161  
; PRIOR FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: JP 2001/246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2430  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1913  
; LENGTH: 3532  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: source  
; LOCATION: (1)..(3532)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (201)..(437)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2622)..(3332)  
; US-10-017-161-1913  
Query Match 3.4%; Score 48; DB 6; Length 3532;  
Best Local Similarity 44.0%; Pred. No. 0.17; Indels 0; Gaps 0;  
Matches 204; Conservative 0; Mismatches 260;  
Qy 513 TGATGATGCAGTAACACTACTGATTATGTTAGATCATTCACAGAAATGTTTAAATAGACT 572  
Db 2639 TGT 2698  
Qy 573 TAACCTTTTACTATAATGTTAAATGTTAACTCCTTTCAATCCAGTAAAGCTTAATG 632  
Db 2699 TGATGTAATGATGACGGTGATTATAGTATAATGATGTTGATGATGATGATGATGATG 2758  
Qy 633 CACACCTTGTCCGCCAATTAACCTGCTAATGTTCTTAAGCTACTTTAGGTAATGATGC 692  
Db 2759 TGTGCTGATGTTGGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2818  
Qy 693 TACAATAACCGCAATAATGTAACGTTGCATGCCCTGATGGTACTATAAGTGTCTGGAGT 752  
Db 2819 TGATGATGATGTTGATCACGGTGATGTTGATGATGATGATGATGATGATGATGATGATG 2878  
Qy 753 AAATAATGTTGGTAGCACAAACACTGAATGTTCTTAACTTCTTAACTTTTACAATAA 812  
Db 2879 TGATAATGTTGATGTTAAATGTTAAATGTTAAATGTTAAATGTTAAATGTTAAATGTT 2938  
Qy 813 TAATGCTCTCTAAATTTCAATCCAGGTAATAGTACATGCCCTTACCTTACCTTACCTTAC 872  
Db 2939 TGACGGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2998  
Qy 873 TTATGTTGTTGAAGCCACTGCAGGTGTTGCCGCTACTTTAGCCAAATAATGTAATATTC 932  
Db 2999 TGATGTTGATGTTGATAGTATAACCGTGTGATGATGATGATGATGATGATGATGATGATG 3058  
Qy 933 ATGCCCTGATGCTACTCAATTTCTAGTGGAGCAACTAATTAATG 976  
Db 3059 TGTTGATGGTGGTGTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATG 3102  
RESULT 10  
US-10-144-771-4707/c  
; Sequence 4707, Application US/10144771  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF  
; FILE REFERENCE: CL001321  
; CURRENT APPLICATION NUMBER: US/10/144,771  
; CURRENT FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 47235  
; SEQ ID NO 4707





[illegible]

**Qy**   948 TCGAATTCCTAGTGGACCAACTAAATTATG 976  
       || | || | || | ||  
**Db**   1226 TCGTGCTGGTTGTGCTAGTAGTG GTG 1254

RESULT 13  
US-10-194-046-l/c  
; Sequence l, Application US/10194046  
; GENERAL INFORMATION:  
; APPLICANT : Robertson, Erle S.  
; TITLE OF INVENTION : LANA Viral Protein Binding Sites  
; FILE REFERENCE : UM-07142  
; CURRENT APPLICATION NUMBER : US/10/194,046  
; CURRENT FILING DATE : 2002-07-11  
; PRIOR APPLICATION NUMBER : 09/410,399  
; PRIOR FILING DATE : 1999-10-01  
; NUMBER OF SEQ ID NOS : 22  
; SOFTWARE : PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH : 3489  
; TYPE : DNA  
; ORGANISM : Kaposi's sarcoma-associated herpesvirus  
US-10-194-046-1

	Query Match	Best Local Similarity	Mismatches	Score	Pred.	No.	Gaps
			Matches	%			
	592 AATAATGGTAATFACGCCCTTTCAATCCAGGTAAAGAATTAATGCACACCCTGTGTCGGCAA TT 651	3.3%; DB 6;	Indels	Length 3489;			
	2473 ACTCCTGCTCCTGCTCCTCTAACCTACCTGCTGCTCCTCTAACCTCCTCTGA CTCTGCTGCT 2414	44.0%;	Mismatches	247;			
	652 AAACCTGCTTAAGTCTTAAGCTACTTTAGGTAAATGATGCTACACAATAACCGCATAA TG 711	0;	Conservative	0;			
	2413 CTAACCTCTGCTCCTGCTCCTCTAACCTACCTGCTCCTGCTCCTCTAACCTCCT GA TAGCTGCTGCT 2354						
	712 AACGTTGTCATGCGCTGATGCTACTATAAGTGTCGTGGAGTAAATTAATTTGGGTAGCACAAA 771						
	2353 CCTCTAACCTCCTGCTCCTGATCCTCTAACCTGCTGCTCCTCTAACCTCCTGCTGCT 2294						
	772 AACACCTGAATGACTAAATTTGCTGCTCCTAACCTTTACAATAAATGCTCCTCAATTTCA AT 831						
	2293 GCTGCTCCTGCTGCTGCTGCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT CAT 2234						
	832 CCAGGTAAATAGTACATGCGCTTACCTTGCCAGCAAAAAAAGATPATGGTGTGAAGCCA CT 891						
	2233 CGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT GCAT 951						
	892 GCAGGTGGTCCCCTACTTTAGCCAAATAATGTAATTTGCATGCCCTGATGGTACTGCA 951						
	2173 GCTGCTGCTCATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2114						
	952 ATTGCTAGTGGACCACTAATTTATTAATATTATAACAGAATGCTTAATTTGCTGCTGCT 1011						
	2113 CATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2054						
	1012 AACCTTTTTTATTTTGATGGTAAT 1032						
	2053 GCTCATCCTGCTGCTGCTCAT 2033						

RESULT 14  
US-10-092-411A-2243  
; Sequence 2243, Application US/10092411A  
; GENERAL INFORMATION:  
; APPLICANT : Lynn Doucette-Stamm et al  
; TITLE OF INVENTION : NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCI  
; TITLE OF INVENTION : EPIDERMIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE : 032796-101  
; CURRENT APPLICATION NUMBER : US/10/092,411A  
; CURRENT FILING DATE : 2002-03-07  
; PRIOR APPLICATION NUMBER : US 09/134,001  
; PRIOR FILING DATE : 1998-08-13



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; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5676
; SEQ ID NO 2243
; LENGTH: 11091
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-2243

Query Match      3.3%; Score 45.8; DB 6; Length 11091;
Best Local Similarity 46.9%; Pred. No. 0.63;
Matches 143; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

QY 726 TGATGGTACTATAGTCTCTCGAGTAAATAATTTGGGTAGCACAAAACACTGAATGTAC 785
Db 3906 TGATGGTATTTGTGAGTGTGGTAGACAAAAGCATAAATGCAATTACACCTGTACATCAAT 3965
QY 786 TAATTTGCTCTTAACCTTTTACAAATAATAATGCTCCTAATTTCAATCCAGGTAAATGTAC 845
Db 3966 TAAAGAAATGCTTAAATATGATATGATTAAGCAGCTGATAGAAAATAAAATTTCA 4025
QY 846 ATGCTACCTTGGCCAGCAAAATAAGATTATGGTGTGAGCCACTGCAGGTGGTCCGC 905
Db 4026 AAGAATAAATGTGCTACAGATGACAAAATTCAGAAGCGAATCCTAAAATTTGAAGAAGC 4085
QY 906 TACTTTAGCCAAATAATGTAATTTGCATGCCCTGATGCTGCTAATTTTATTTTGA 1025
Db 4086 TAGATTGAAGCAAAAGTAATTTCAAGCAATAGTACTAGAGATCAAGTAAATGAAGC 4145
QY 966 AACTAATATGTAATATTATAACAGAAATGCTCTAATTTGCTGCTAATTTTATTTTGA 1025
Db 4146 GAAACTAATGGAATAATAATAAGAAATATACACCAGCACTACTGTGAATCTGA 4205
QY 1026 TGGTA 1030
Db 4206 AGCTA 4210

RESULT 15
US-09-949-004-601
; Sequence 601, Application US/09949004
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR GENES ASSOCIATED WITH DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000848
; CURRENT APPLICATION NUMBER: US/09/949,004
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 60/232,045
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 6961
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 601
; LENGTH: 21423
; TYPE: DNA
; ORGANISM: Human
US-09-949-004-601
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Query Match      3.2%; Score 45; DB 5; Length 21423;
Best Local Similarity 45.4%; Pred. No. 1.1;
Matches 250; Conservative 0; Mismatches 290; Indels 11; Gaps 2;

QY 498 TACTGGTACTGCACCTTGTATGATGGAGTAACCTACTGATTATGTAGATCATTCACAGAATG 557
Db 19722 TAATGGTATGATGCTGTGATGAGGTGATATGATGAAGATGATGAATAAGGTAATGAAT 19781
QY 558 TGTTAAATGTAGACTTAACTTTTACTATAATATGTTAATGTTAATGTTAATCTCTTCAATCC 617
Db 19782 TCATGATGGTGAAGGTGATGTTAATGTTGATGGTGAAGGTGATGATCAAGATGATGA 19841
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QY 618 AGGTAAAGTTAATGCACACCTTGTTCGGCAATTTAAACCTGCCTAAATGTTGCTTAAGCTAC 677
Db 19842 CAATGAAGGTGATGATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 19901
QY 678 TTTAGGTAAATGCTACATAACCCGATTAATTAACGTTGCGATGCCCTGATGGTACTAT 737
Db 19902 TGGAAACGAGCATGGTAAAGTAGCGGTGATGATTTAAATGATCATGATGATGATGATGATG 19961
QY 738 AAGTGTGCTGGAGTAAATAATTTGGGTAGCACAAAACACTGAATGTACTAATTTGCTCC 797
Db 19962 TGGTGTGTTGATGAAGGTGATGTTAGTGAAGGTGATGATGAAGGTGATGTTAGTGGTGG 20021
QY 798 TAACTTTTACAATAATAATGCTCCTAATTTTCA--ATCCAGGTAAATAGTACATGCCTACCT 855
Db 20022 TGATAGTGTGATGAAAGTAATGTGAAGGTGATGATGAAGGTGATGATGATGATGATGAT 20081
QY 856 TGCCAGCAAAATAAGATTATGCTGCTGAAGCCACTGCAGGTGGTGGCCCTACTTTAGCC 915
Db 20082 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 20132
QY 916 AATAATATGTAATATTGTCATGCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 975
Db 20133 GATGAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 20192
QY 976 GTAAATATTATAACAGAAATGCTCTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1035
Db 20193 GATAAAGGTGATAATGAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 20252
QY 1036 TTCTAGGCCAGG 1046
Db 20253 GATGATGAAGG 20263
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Search completed: February 17, 2003, 01:52:57  
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